



SEQUENCE LISTING

<110> Andersson, Leif
Luthman, L. Holger
Marklund, Stefan

#6

<120> VARIANTS OF THE HUMAN AMP-ACTIVATED PROTEIN KINASE GAMMA 3 SUBUNIT

<130> 11145-007001

<140> US 09/826,581

<141> 2001-04-05

<150> US 60/195,665

<151> 2000-04-07

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 821

<212> DNA

<213> Homo sapiens

<400> 1

tctgagagcc caactctgct caatgaccat gttccacat gctccaagcc acatcccctc 60
aaaaagggtc cctctagctt gtcctcagtg acccaggagg cagctgagga ccaagtaccc 120
agattatccg gtgcgcccct tccctcccag caacccccag ccttcagggc tgtagcagct 180
gagcaaattg gggcccctcc ctctcattgc ctgacaccca atcagagaga aaccgatcct 240
ggcagggcag ggtgcccggg gccgggcccga gaatagtgcg gccagccac agtgtcgcac 300
acttgctctc agttggctctg gggctggcca catggagccc gggctggagc acgactgog 360
cagggatatg gggctccagg ggagccggag ccggggcagc tgaggccaga agattgagcg 420
cacgggctgt gaattgtgtg gtgggcgtgt gtgtcttctg gtgtgtgttt ggtctggatt 480
ttctcgtgaa tatgggcatg tgcattgttg ggcataatgta ttgtgagtgt gtgtggttct 540
gtgtgccttg gagtgttttg atgtgtgtgt ttctgtgtgt gtttgtgtat ggctgcattg 600
ctgtgtatgg cgtgtgtctg agcgtgtgta ttgggtgtgca tgggtgtgta ggcgtgtgtt 660
cagggagaag ggggttgagg atgtaaggca ctttccccac tccttcagaa actcttctcc 720
ccacagaccc ctctctggag cagccttggg ggttctgagc atcaaggtag ggagaatgcc 780
ccctccctgg ggcctaacct cttccccac ttccttgctc c 821

<210> 2

<211> 989

<212> DNA

<213> Homo sapiens

<400> 2

caggccccat tccccttcca gagatgagct tcttagagca agaaaacagc agctcatggc 60
catcaccagc tgtgaccagc agctcagaaa gaatccgtgg gaaacggagg gccaaagcct 120
tgagatggac aaggcagaag tcgggtggagg aaggggagcc accaggtcag ggggaagggtg 180
aggccaaggc cagttctggg gaggtgggag ccaggggagt gggaaatccc agaggagcct 240
gggtctggtc tctacctcag gtccctccat aacacagagt tggacccaac cttcatcttg 300
tggcctcagt ctccctacat agtagagaac aaggcactgc agtgccagag gccagcatgg 360

ccaactcaga	aagatgggac	agagccacta	cctggggcga	ctctcaggtc	agccccctcac	420
ctgcaaatag	ggccacagca	tccaggcttc	ccactgctgc	tgtgagatga	atggcgacag	480
cagatgagaa	cgtgcttttg	aagatggagt	tactgtcctc	ttccccctcct	cccccaaaca	540
ggtccccggt	ccaggccagc	tgctgagtc	accgggctgg	aggccacatt	ccccaaagacc	600
acacccttgg	ctcaagctga	tccctgccggg	gtgggcactc	caccaacagg	gtgggactgc	660
ctccccctctg	actgtacagc	ctcagctgca	ggctccagca	cagatgatgt	ggagctggcc	720
acggagttcc	cagccacaga	ggcctgggag	tgtgagctag	aaggcctgct	ggaagagagg	780
cctgccctgt	gcctgtcccc	gcaggcccca	tttcccaagc	tgggctggga	tgacgaactg	840
cggaaacccg	gcgcccagat	ctacatgcgc	ttcatgcagg	agcacacctg	ctacgatgcc	900
atggcaacta	gctccaagct	agtcattcttc	gacaccatgc	tggaggtgag	gccacggctc	960
tgcccaacct	gtactcactc	tccatccac				989

<210> 3

<211> 1722

<212> DNA

<213> Homo sapiens

<400> 3

cctggccccct	cagatcaaga	aggccttctt	tgtcttgggtg	gccaacgggtg	tgccgggcagc	60
ccctctatgg	gacagcaaga	agcagagctt	tgtgggtgag	gagaggctgg	ggaggtgaag	120
ggagatggag	gaggtgaggg	ggagatcttg	tacggttggt	ctggggctga	tctctgatat	180
accacaagct	tggcttcagg	ccaagcccag	ccaggggcca	gggtggagga	aagtccatcc	240
ggagtctgca	tggccagctg	ggagaccctg	gggtcaatt	tccccatctg	tggagccgct	300
atgaccagct	gacacctttc	acctccgcta	ctgcatggcc	ctgtgccata	ggtgctaggg	360
agcaaatggg	gggaggcagg	agagaaagag	ccccacttct	caggcctggg	gggtgcccc	420
actgtcctgt	tcccacagtc	cccactgtgt	ctcagcacia	ggacactggc	aggggtggga	480
gggatctga	ccctcaacct	gccttccacc	caaaggcccc	gggtgacct	cctccccgcc	540
cctccccctg	agggatgctg	accatcactg	acttcactct	ggtgctgcat	cgtactaca	600
ggtccccct	ggtgaggagt	gggtgggaa	tcttatgggc	accagagggg	gcgggggcgg	660
aggggagtcc	tcttgagacc	tgggtgcccta	gaagcccacg	tctttctgac	ttctggagtc	720
ctgtcagatg	ctctagggtcc	agatctatga	gattgaacaa	cataagattg	agacctggag	780
gggtgagtgg	ggagaggaac	ccggaaaggg	gctgttgggtg	atggtgggcc	agggcttaag	840
gtggaggatg	ggcagtgggg	atgtcctgga	gtgaacaggg	gagggacaat	aggagcctcg	900
ggtgcctgac	ggaagggaag	ctgcctggga	ctgcaagggtg	aggcagggtga	cgggctcccc	960
tggcctgact	ctggctcttt	ctgcagagat	ctacctgcaa	ggctgcttca	agcctctggt	1020
ctccatctct	cctaattgata	ggtgggtgtc	tctgtctcatt	cacctgagcc	tcctcctccc	1080
acagtccccct	tccccagtc	cactcagctc	tgaactcacc	tcttcactct	aggcggcaca	1140
cagacaaggg	agccttggtg	ccctgccctc	ctttttaggg	gcctgggatg	gaggttgtct	1200
ctccctaggg	tgccccgagg	ctcactgctc	ccatctctgc	agcctgtttg	aagctgtcta	1260
caccctcatc	aagaaccgga	tccatgcct	gcctgttctt	gacccgggtg	caggcaacgt	1320
actccacatc	ctcacacaca	aacgcctgct	caagttcctg	cacatctttg	taagcctggg	1380
cccagggtggg	aggaaggggg	agacctgggc	aggtgatcag	agggcctgag	gagtcttcag	1440
ccctagcagt	cgtggggaag	agctgggagc	cctcttgaag	ctgctggatc	cctgatctcc	1500
acctggtccc	catcctaacc	agggttccct	gctgccccgg	ccctccttcc	tctaccgcac	1560
tatccaagat	ttgggcatcg	gcacattccg	agacttggct	gtgggtgctg	agacagcacc	1620
catcctgact	gcaactggaca	tctttgtgga	ccggcgtgtg	tctgcactgc	ctgtggtcaa	1680
cgaatgtggg	acccaccccc	aggatgagag	gctcgggctg	ga		1722

<210> 4

<211> 1014

<212> DNA

<213> Homo sapiens

<210> 5

<211> 1647

<212> DNA

<213> Homo sapiens

$\langle 220 \rangle$

<221> CDS

<222> (20) ... (1486)

<400> 5

acc cct tcc tgg agc agc ctt ggg ggt tct gag cat caa gag atg agc 100
Thr Pro Ser Trp Ser Ser Leu Gly Gly Ser Glu His Gln Glu Met Ser
15 20 25

agc agc tca gaa aga atc cgt ggg aaa cgg agg gcc aaa gcc ttg aga 196
 Ser Ser Ser Glu Arg Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg
 45 50 55

gaa ggt ccc cgg tcc agg cca gct gct gag tcc acc ggg ctg gag gcc 292
Glu Gly Pro Arg Ser Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala
80 85 90

aca ttc ccc aag acc aca ccc ttg gct caa gct gat cct gcc ggg gtg Thr Phe Pro Lys Thr Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val 95 100 105	340
ggc act cca cca aca ggg tgg gac tgc ctc ccc tct gac tgt aca gcc Gly Thr Pro Pro Thr Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala 110 115 120	388
tca gct gca ggc tcc agc aca gat gat gtg gag ctg gcc acg gag ttc Ser Ala Ala Gly Ser Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe 125 130 135	436
cca gcc aca gag gcc tgg gag tgt gag cta gaa ggc ctg ctg gaa gag Pro Ala Thr Glu Ala Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu 140 145 150 155	484
agg cct gcc ctg tgc ctg tcc ccg cag gcc cca ttt ccc aag ctg ggc Arg Pro Ala Leu Cys Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly 160 165 170	532
tgg gat gac gaa ctg cgg aaa ccc ggc gcc cag atc tac atg cgc ttc Trp Asp Asp Glu Leu Arg Lys Pro Gly Ala Gln Ile Tyr Met Arg Phe 175 180 185	580
atg cag gag cac acc tgc tac gat gcc atg gca act agc tcc aag cta Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys Leu 190 195 200	628
gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt gct ctg Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe Ala Leu 205 210 215	676
gtg gcc aac ggt gtg cgg gca gcc cct cta tgg gac agc aag aag cag Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln 220 225 230 235	724
agc ttt gtg ggg atg ctg acc atc act gac ttc atc ctg gtg ctg cat Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val Leu His 240 245 250	772
cgc tac tac agg tcc ccc ctg gtc cag atc tat gag att gaa caa cat Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His 255 260 265	820
aag att gag acc tgg agg gag atc tac ctg caa ggc tgc ttc aag cct Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro 270 275 280	868
ctg gtc tcc atc tct cct aat gat agc ctg ttt gaa gct gtc tac acc Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr 285 290 295	916
ctc atc aag aac cgg atc cat cgc ctg cct gtt ctt gac ccg gtg tca	964

Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro Val Ser	
300 305 310 315	
ggc aac gta ctc cac atc ctc aca cac aaa cgc ctg ctc aag ttc ctg	1012
Gly Asn Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu	
320 325 330	
cac atc ttt ggt tcc ctg ctg ccc cgg ccc tcc ttc ctc tac cgc act	1060
His Ile Phe Gly Ser Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr	
335 340 345	
atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gct gtg gtg ctg	1108
Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu	
350 355 360	
gag aca gca ccc atc ctg act gca ctg gac atc ttt gtg gac cgg cgt	1156
Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg	
365 370 375	
gtg tct gca ctg cct gtg gtc aac gaa tgt ggt cag gtc gtg ggc ctc	1204
Val Ser Ala Leu Pro Val Val Asn Glu Cys Gly Gln Val Val Gly Leu	
380 385 390 395	
tat tcc cgc ttt gat gtg att cac ctg gct gcc cag caa acc tac aac	1252
Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr Tyr Asn	
400 405 410	
cac ctg gac atg agt gtg gga gaa gcc ctg agg cag agg aca cta tgt	1300
His Leu Asp Met Ser Val Gly Glu Ala Leu Arg Gln Arg Thr Leu Cys	
415 420 425	
ctg gag gga gtc ctt tcc tgc cag ccc cac gag agc ttg ggg gaa gtg	1348
Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Ser Leu Gly Glu Val	
430 435 440	
atc gac agg att gct cgg gag cag gta cac agg ctg gtg cta gtg gac	1396
Ile Asp Arg Ile Ala Arg Glu Gln Val His Arg Leu Val Leu Val Asp	
445 450 455	
gag acc cag cat ctc ttg ggc gtg gtc tcc ctc tcc gac atc ctt cag	1444
Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile Leu Gln	
460 465 470 475	
gca ctg gtg ctc agc cct gct ggc atc gat gcc ctc ggg gcc	1486
Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	
480 485	
tgagaagatc tgagtccctca atcccaagcc acctgcacac ctggaagcca atgaaggga	1546
ctggagaact cagccttcat cttccccac cccatttgc tggttcagct atgattcagg	1606
taggctctgc cctgggccaat gacaccagcc tcttagtctt c	1647

<210> 6

<211> 489

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Glu Pro Gly Leu Glu His Ala Leu Arg Arg Thr Pro Ser Trp Ser
 1              5              10              15
Ser Leu Gly Gly Ser Glu His Gln Glu Met Ser Phe Leu Glu Gln Glu
      20              25              30
Asn Ser Ser Ser Trp Pro Ser Pro Ala Val Thr Ser Ser Glu Arg
      35              40              45
Ile Arg Gly Lys Arg Arg Ala Lys Ala Leu Arg Trp Thr Arg Gln Lys
      50              55              60
Ser Val Glu Glu Gly Glu Pro Pro Gly Gln Gly Glu Gly Pro Arg Ser
65              70              75              80
Arg Pro Ala Ala Glu Ser Thr Gly Leu Glu Ala Thr Phe Pro Lys Thr
      85              90              95
Thr Pro Leu Ala Gln Ala Asp Pro Ala Gly Val Gly Thr Pro Pro Thr
      100              105              110
Gly Trp Asp Cys Leu Pro Ser Asp Cys Thr Ala Ser Ala Ala Gly Ser
      115              120              125
Ser Thr Asp Asp Val Glu Leu Ala Thr Glu Phe Pro Ala Thr Glu Ala
      130              135              140
Trp Glu Cys Glu Leu Glu Gly Leu Leu Glu Glu Arg Pro Ala Leu Cys
145              150              155              160
Leu Ser Pro Gln Ala Pro Phe Pro Lys Leu Gly Trp Asp Asp Glu Leu
      165              170              175
Arg Lys Pro Gly Ala Gln Ile Tyr Met Arg Phe Met Gln Glu His Thr
      180              185              190
Cys Tyr Asp Ala Met Ala Thr Ser Ser Lys Leu Val Ile Phe Asp Thr
      195              200              205
Met Leu Glu Ile Lys Lys Ala Phe Phe Ala Leu Val Ala Asn Gly Val
      210              215              220
Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln Ser Phe Val Gly Met
225              230              235              240
Leu Thr Ile Thr Asp Phe Ile Leu Val Leu His Arg Tyr Tyr Arg Ser
      245              250              255
Pro Leu Val Gln Ile Tyr Glu Ile Glu Gln His Lys Ile Glu Thr Trp
      260              265              270
Arg Glu Ile Tyr Leu Gln Gly Cys Phe Lys Pro Leu Val Ser Ile Ser
      275              280              285
Pro Asn Asp Ser Leu Phe Glu Ala Val Tyr Thr Leu Ile Lys Asn Arg
      290              295              300
Ile His Arg Leu Pro Val Leu Asp Pro Val Ser Gly Asn Val Leu His
305              310              315              320
Ile Leu Thr His Lys Arg Leu Leu Lys Phe Leu His Ile Phe Gly Ser
      325              330              335

Leu Leu Pro Arg Pro Ser Phe Leu Tyr Arg Thr Ile Gln Asp Leu Gly
      340              345              350
Ile Gly Thr Phe Arg Asp Leu Ala Val Val Leu Glu Thr Ala Pro Ile
      355              360              365
Leu Thr Ala Leu Asp Ile Phe Val Asp Arg Arg Val Ser Ala Leu Pro
      370              375              380
Val Val Asn Glu Cys Gly Gln Val Val Gly Leu Tyr Ser Arg Phe Asp

```

385		390		395		400									
Val	Ile	His	Leu	Ala	Ala	Gln	Gln	Thr	Tyr	Asn	His	Leu	Asp	Met	Ser
				405					410					415	
Val	Gly	Glu	Ala	Leu	Arg	Gln	Arg	Thr	Leu	Cys	Leu	Glu	Gly	Val	Leu
			420					425					430		
Ser	Cys	Gln	Pro	His	Glu	Ser	Leu	Gly	Glu	Val	Ile	Asp	Arg	Ile	Ala
		435					440					445			
Arg	Glu	Gln	Val	His	Arg	Leu	Val	Leu	Val	Asp	Glu	Thr	Gln	His	Leu
	450					455				460					
Leu	Gly	Val	Val	Ser	Leu	Ser	Asp	Ile	Leu	Gln	Ala	Leu	Val	Leu	Ser
465					470				475					480	
Pro	Ala	Gly	Ile	Asp	Ala	Leu	Gly	Ala							
				485											

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 7
 aggctcttgg aataggggct cagg

24

<210> 8
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 8
 agggaattgg ggtcccagaa aagtg

25

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 9
 gaattgattt tgatgcatta ctcc

24

<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetically generated primer

<400> 10
agtggcggct gcagcaccgt

20

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 11
aggcagatgg gaggtgcgca ctgag

25

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 12
acagggatgg catgagaaac cctgc

25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 13
ttctggtagt ggcaccctga tgcaa

25

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetically generated primer

<400> 14
gacctgtgag tccttacact tgcag

25